

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,902
Source: PCT
Date Processed by STIC: 06-22-2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,902

TIME: 10:32:46

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538902.raw

3 <110> APPLICANT: University of Medicine and Dentistry of New Jersey
 4 Kaplan, Jeffrey B.
 6 <120> TITLE OF INVENTION: Compositions and Methods for Enzymatic Detachment of
 Bacterial and Fungal
 7 Biofilms
 9 <130> FILE REFERENCE: UMD-0015
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,902
 C--> 11 <141> CURRENT FILING DATE: 2005-06-14
 11 <150> PRIOR APPLICATION NUMBER: US 60/435,817
 12 <151> PRIOR FILING DATE: 2002-12-20
 14 <160> NUMBER OF SEQ ID NOS: 15
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1146
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
 23 <400> SEQUENCE: 1
 24 atgaattata ttaagaaaat tatttttatct cttttcctac tgggactatt tagcgtgttg 60
 26 aattgttgcg taaaaggcaa ttccatatat ccgcaaaaaa caagtaccaa gcagaccgga 120
 28 ttaatgctgg acatcgcccg acattttttat tcacccgagg tgattaaatc ctttattgat 180
 30 accatcagcc tttccggcgg taattttctg cacctgcatt tttccgacca tgaaaactat 240
 32 gcgatagaaa gccatttact taatcaacgt gcggaaaatg ccgtgcaggg caaagacggt 300
 34 atttatatta atccttatac cggaaagcca ttcttgagtt atcggcaact tgacgatatc 360
 36 aaagcctatg ctaaggcaaa aggcattgag ttgattcccg aacttgacag cccgaatcac 420
 38 atgacggcga tctttaaact ggtgcaaaaa gacagagggg tcaagtacct tcaaggatta 480
 40 aaatcacgcc aggtagatga tgaaattgat attactaatg ctgacagtat tacttttatg 540
 42 caatctttta tgagtgggt tattgatatt tttggcgaca cgagtcagca ttttcattat 600
 44 ggtggcgatg aatttggtta ttctgtggaa agtaatcatg agtttattac gtatgccaat 660
 46 aaactatcct actttttaga gaaaaaaggg ttgaaaaccc gaatgtggaa tgacggatta 720
 48 attaaaaata cttttgagca aatcaaccgg aatattgaaa ttacttattg gagctatgat 780
 50 ggcgatacgc aggacaaaaa tgaagctgcc gagcgccgtg atatgcgggt cagtttgccg 840
 52 gagttgctgg cgaaaggcct tactgtcctg aactataatt cctattatct ttacattggt 900
 54 ccgaaagctt caccaacctt ctgcgaagat gccgcctttg ccgccaaaga tgttataaaa 960
 56 aattgggatc ttggtgtttg ggatggacga aacacaaaaa accgcgtaca aaatactcat 1020
 58 gaaatagccg gcgcagcatt atcgatctgg ggagaagatg caaagcgct gaaagacgaa 1080
 60 acaattcaga aaaacacgaa aggtttattg gaagcgggtga ttcataagac gaatggggat 1140
 62 gagtga 1146
 65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 381
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
 70 <400> SEQUENCE: 2
 72 Met Asn Tyr Ile Lys Lys Ile Ile Leu Ser Leu Phe Leu Leu Gly Leu
 73 1 5 10 15

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76 Phe Ser Val Leu Asn Cys Cys Val Lys Gly Asn Ser Ile Tyr Pro Gln
77          20          25          30
80 Lys Thr Ser Thr Lys Gln Thr Gly Leu Met Leu Asp Ile Ala Arg His
81          35          40          45
84 Phe Tyr Ser Pro Glu Val Ile Lys Ser Phe Ile Asp Thr Ile Ser Leu
85          50          55          60
88 Ser Gly Gly Asn Phe Leu His Leu His Phe Ser Asp His Glu Asn Tyr
89 65          70          75          80
92 Ala Ile Glu Ser His Leu Leu Asn Gln Arg Ala Glu Asn Ala Val Gln
93          85          90          95
96 Gly Lys Asp Gly Ile Tyr Ile Asn Pro Tyr Thr Gly Lys Pro Phe Leu
97          100          105          110
100 Ser Tyr Arg Gln Leu Asp Asp Ile Lys Ala Tyr Ala Lys Ala Lys Gly
101          115          120          125
104 Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn His Met Thr Ala Ile
105          130          135          140
108 Phe Lys Leu Val Gln Lys Asp Arg Gly Val Lys Tyr Leu Gln Gly Leu
109 145          150          155          160
112 Lys Ser Arg Gln Val Asp Asp Glu Ile Asp Ile Thr Asn Ala Asp Ser
113          165          170          175
116 Ile Thr Phe Met Gln Ser Leu Met Ser Glu Val Ile Asp Ile Phe Gly
117          180          185          190
120 Asp Thr Ser Gln His Phe His Ile Gly Gly Asp Glu Phe Gly Tyr Ser
121          195          200          205
124 Val Glu Ser Asn His Glu Phe Ile Thr Tyr Ala Asn Lys Leu Ser Tyr
125          210          215          220
128 Phe Leu Glu Lys Lys Gly Leu Lys Thr Arg Met Trp Asn Asp Gly Leu
129 225          230          235          240
132 Ile Lys Asn Thr Phe Glu Gln Ile Asn Pro Asn Ile Glu Ile Thr Tyr
133          245          250          255
136 Trp Ser Tyr Asp Gly Asp Thr Gln Asp Lys Asn Glu Ala Ala Glu Arg
137          260          265          270
140 Arg Asp Met Arg Val Ser Leu Pro Glu Leu Leu Ala Lys Gly Phe Thr
141          275          280          285
144 Val Leu Asn Tyr Asn Ser Tyr Tyr Leu Tyr Ile Val Pro Lys Ala Ser
145          290          295          300
148 Pro Thr Phe Ser Gln Asp Ala Ala Phe Ala Ala Lys Asp Val Ile Lys
149 305          310          315          320
152 Asn Trp Asp Leu Gly Val Trp Asp Gly Arg Asn Thr Lys Asn Arg Val
153          325          330          335
156 Gln Asn Thr His Glu Ile Ala Gly Ala Ala Leu Ser Ile Trp Gly Glu
157          340          345          350
160 Asp Ala Lys Ala Leu Lys Asp Glu Thr Ile Gln Lys Asn Thr Lys Ser
161          355          360          365
164 Leu Leu Glu Ala Val Ile His Lys Thr Asn Gly Asp Glu
165          370          375          380
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 555
170 <212> TYPE: DNA

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171 <213> ORGANISM: Actinobacillus ligniersii strain 19393
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176 gagaaaaacg gaacctatatt caatccgaaa acaaataagc cgtttctcac ttataaacag      120
178 ctcaatgaaa ttatctatta tgccaaagaa cgaaatattg aaattgtgcc tgaagtogat      180
180 agcccgaatc atatgacggc gatttttgat cttttaaccc ttaagcacgg taaggagtat      240
182 gtgaaagggc tgaaatcgcc ttatcttgcc gaggaatcg atattaataa ccctgaagcg      300
184 gttgaaatta tcaaacctt aatcggtgaa gtgatttata tttttgggca ttccagccga      360
186 cactttcata tcggcggaga cgaatttagt tatgcggtcg aaaacaatca cgaatttatt      420
188 cgttatgtaa atacgctaaa tgactttatt aataacaaag gactaattac ccgtatttgg      480
190 aacgacgggt tgattaaaaa caatttaa at gagcttaatc ggaatatcga aattacttat      540
192 tggagctacg acggt                                     555
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 185
197 <212> TYPE: PRT
198 <213> ORGANISM: Actinobacillus ligniersii strain 19393
200 <400> SEQUENCE: 4
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203 1          5          10          15
206 Glu Asn Ala Val Glu Lys Asn Gly Thr Tyr Phe Asn Pro Lys Thr Asn
207          20          25          30
210 Lys Pro Phe Leu Thr Tyr Lys Gln Leu Asn Glu Ile Ile Tyr Tyr Ala
211          35          40          45
214 Lys Glu Arg Asn Ile Glu Ile Val Pro Glu Val Asp Ser Pro Asn His
215          50          55          60
218 Met Thr Ala Ile Phe Asp Leu Leu Thr Leu Lys His Gly Lys Glu Tyr
219 65          70          75          80
222 Val Lys Gly Leu Lys Ser Pro Tyr Leu Ala Glu Glu Ile Asp Ile Asn
223          85          90          95
226 Asn Pro Glu Ala Val Glu Ile Ile Lys Thr Leu Ile Gly Glu Val Ile
227          100         105         110
230 Tyr Ile Phe Gly His Ser Ser Arg His Phe His Ile Gly Gly Asp Glu
231          115         120         125
234 Phe Ser Tyr Ala Val Glu Asn Asn His Glu Phe Ile Arg Tyr Val Asn
235          130         135         140
238 Thr Leu Asn Asp Phe Ile Asn Asn Lys Gly Leu Ile Thr Arg Ile Trp
239 145         150         155         160
242 Asn Asp Gly Leu Ile Lys Asn Asn Leu Asn Glu Leu Asn Arg Asn Ile
243          165         170         175
246 Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
247          180         185
250 <210> SEQ ID NO: 5
251 <211> LENGTH: 558
252 <212> TYPE: DNA
253 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain IDH781
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258 cagggcaaag acggtattta tattaatcct tataccggaa agccattctt gagttatcga      120
260 caacttgacg atatcaaagc ctatgctaag gcaaaaggca ttgagttgat tcccgaactt      180

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262 gatagtccga atcacatgac ggcgatcttt aaactgggtgc aaaaagacag agggatcaag      240
264 tatcttcaag gattaaaatc acgccaggta gatgatgaaa ttgatattac taatgctgac      300
266 agtattgctt ttatgcaatc tttaatgagt gaggttattg atatttttgg cgacacgagt      360
268 cagcattttc atattgggtg cgatgaattt gggttattctg tggaaagtaa tcatgagttt      420
270 attacgtatg ccaataaact atcctacttt ttagagaaaa aggggttgaa aaccggaatg      480
272 tggaatgacg gattaattaa aagtactttt gagcaaatca acccgaatat tgaaattact      540
274 tattggagct atgatggc                                     558
277 <210> SEQ ID NO: 6
278 <211> LENGTH: 186
279 <212> TYPE: PRT
280 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain IDH781
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285 1      5      10      15
288 Glu Asn Ala Val Gln Gly Lys Asp Gly Ile Tyr Ile Asn Pro Tyr Thr
289      20      25      30
292 Gly Lys Pro Phe Leu Ser Tyr Arg Gln Leu Asp Asp Ile Lys Ala Tyr
293      35      40      45
296 Ala Lys Ala Lys Gly Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn
297      50      55      60
300 His Met Thr Ala Ile Phe Lys Leu Val Gln Lys Asp Arg Gly Ile Lys
301 65      70      75      80
304 Tyr Leu Gln Gly Leu Lys Ser Arg Gln Val Asp Asp Glu Ile Asp Ile
305      85      90      95
308 Thr Asn Ala Asp Ser Ile Ala Phe Met Gln Ser Leu Met Ser Glu Val
309      100     105     110
312 Ile Asp Ile Phe Gly Asp Thr Ser Gln His Phe His Ile Gly Gly Asp
313      115     120     125
316 Glu Phe Gly Tyr Ser Val Glu Ser Asn His Glu Phe Ile Thr Tyr Ala
317      130     135     140
320 Asn Lys Leu Ser Tyr Phe Leu Glu Lys Lys Gly Leu Lys Thr Arg Met
321 145     150     155     160
324 Trp Asn Asp Gly Leu Ile Lys Ser Thr Phe Glu Gln Ile Asn Pro Asn
325      165     170     175
328 Ile Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
329      180     185
332 <210> SEQ ID NO: 7
333 <211> LENGTH: 558
334 <212> TYPE: DNA
335 <213> ORGANISM: Haemophilus aphrophilus strain NJ8700
337 <400> SEQUENCE: 7
338 gaccacgaaa attatgcttt agaaagcagg ttgttgaatc agcgggcaga aaacgcaatt      60
340 ttaaataaaaa acggaattta tattaatcct tacaccaata agcctttctt gagttatcaa      120
342 cagttggatg acattaaagc atatgcaaaa ttaaaaggta ttgagcttat tcccgaatta      180
344 gatagcccga atcacatgac agcgattttt accttattaa aaaaagaaaa aggaaaaaat      240
346 tatcttcaat cgttaaaatc accacaaaat gatgaggaaa ttagcattac caatccggac      300
348 agcattgcat ttatgcaatc cttattaaca gaggtaatc atacctttgg cgatagcacc      360
350 aagcattttc atattggcgg agatgagttt gggttatgatg aaaatagtaa tcatgaattt      420
352 attacctatg ccaataaatt ggctgatttt ttaagagaaa aaggattaaa aactcgaatt      480

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354 tggaatgatg gtttaattaa aaataccata gatcaattaa atcctaatat tgaaattacc      540
356 tactggagtt acgacggc      558
359 <210> SEQ ID NO: 8
360 <211> LENGTH: 186
361 <212> TYPE: PRT
362 <213> ORGANISM: Haemophilus aphrophilus strain NJ8700
364 <400> SEQUENCE: 8
366 Asp His Glu Asn Tyr Ala Leu Glu Ser Arg Leu Leu Asn Gln Arg Ala
367 1          5          10          15
370 Glu Asn Ala Ile Leu Asn Lys Asn Gly Ile Tyr Ile Asn Pro Tyr Thr
371          20          25          30
374 Asn Lys Pro Phe Leu Ser Tyr Gln Gln Leu Asp Asp Ile Lys Ala Tyr
375          35          40          45
378 Ala Lys Leu Lys Gly Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn
379          50          55          60
382 His Met Thr Ala Ile Phe Thr Leu Leu Lys Lys Glu Lys Gly Lys Asn
383 65          70          75          80
386 Tyr Leu Gln Ser Leu Lys Ser Pro Gln Asn Asp Glu Glu Ile Ser Ile
387          85          90          95
390 Thr Asn Pro Asp Ser Ile Ala Phe Met Gln Ser Leu Leu Thr Glu Val
391          100         105         110
394 Ile His Thr Phe Gly Asp Ser Thr Lys His Phe His Ile Gly Gly Asp
395          115         120         125
398 Glu Phe Gly Tyr Asp Glu Asn Ser Asn His Glu Phe Ile Thr Tyr Ala
399          130         135         140
402 Asn Lys Leu Ala Asp Phe Leu Arg Glu Lys Gly Leu Lys Thr Arg Ile
403 145         150         155         160
406 Trp Asn Asp Gly Leu Ile Lys Asn Thr Ile Asp Gln Leu Asn Pro Asn
407          165         170         175
410 Ile Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
411          180         185
414 <210> SEQ ID NO: 9
415 <211> LENGTH: 555
416 <212> TYPE: DNA
417 <213> ORGANISM: Actinobacillus pleuropneumoniae strain IA5
419 <400> SEQUENCE: 9
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422 gagaaaaacg gaacctatatt caatccgaaa acaaataagc cgtttctcac ttataaacag      120
424 ctcaatgaaa ttatctatta tgccaaagaa cgaaatattg aaattgtgcc tgaagtcgat      180
426 agcccgaatc atatgacggc gatttttgat cttttaaccc ttaagcacgg aaaggaatac      240
428 gtaaaagggc taaaatcgcc ttatatcgcc gaggaatcg atattaataa ccccgagcg      300
430 gttgaagtta taaaacctt aatcggtgaa gtgatctata ttttcggaca ttcaagccgg      360
432 catttccata tcggcggaga tgaatttagc tatgcggtcg aaaataatca tgaatttatt      420
434 cggtatgtga ataccttaaa tgattttatc aattccaaag ggctaattac ccgtgtttgg      480
436 aatgacgggt tgatcaaaaa caacttaagc gaactcaata aaaacattga aatcacttac      540
438 tggagctacg acggt      555
441 <210> SEQ ID NO: 10
442 <211> LENGTH: 185
443 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/538,902

DATE: 06/22/2005
TIME: 10:32:48

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06222005\J538902.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 1

Seq#:13; N Pos. 3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538902.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0